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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/608,388	06/30/2003	Seishi Kato	2003-0907	7952

7590 04/24/2006

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EXAMINER	
REDDIG, PETER J	

ART UNIT	PAPER NUMBER
1642	

DATE MAILED: 04/24/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/608,388	KATO ET AL.	
	Examiner	Art Unit	
	Peter J. Reddig	1642	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *1/20/2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-4* is/are pending in the application.

4a) Of the above claim(s) *2-4* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☒ Certified copies of the priority documents have been received in Application No. 09/155,008.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *sequence*.

DETAILED ACTION

Election/Restrictions

The response filed on 01/20/2006 to the restriction requirement of 12/20/205 has been received. Applicant has elected Group I, claim 1. Because applicant did not distinctly and specifically point out any supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP 818.03(a). Claims 2-4 are withdrawn from further consideration by the examiner, 37 CFR 1.142(b), as being drawn to a non-elected invention. Thus, claim 1 is pending and is currently under examination.

Specification Objections

The disclosure is objected to because of the following informalities.

The title is objected to in light of the elected claims. A new title is required that is clearly indicative of the invention to which the claims are directed.

The following title is suggested: Human Membrane Antigen TM4 Superfamily Protein.

The abstract of the disclosure is objected to because of the use of the word "said". See MPEP § 608.01(b). Applicant is reminded of the proper language and format for an abstract of the disclosure. The abstract should be in narrative form and generally limited to a single paragraph on a separate sheet within the range of 50 to 150 words. **The form and legal phraseology often used in patent claims, such as "means" and "said," should be avoided**. The abstract should describe the disclosure sufficiently to assist readers in deciding whether there is a need for consulting the full patent text for details.

Appropriate correction is required.

There appears to be several spelling errors in the specification: (page 3, line 20) "obtainment", should be "obtaining"; (page 4, line 20) "culture", should be "cultured"; (page 5, line 13) "possessed", should be "possesses"; (page 7, line 12) "antibodiesusing", should be "antibodies using"; (page 7, line 23) "assay", should be "assays"; (page 16, line 7) "commoncold", should be "common cold"; (page 32, line 1) "ytokines", should be "cytokines"; (page 32, line 28 and 29; page 33, line 1) "effecting", should be "affecting"; (page 35, line 16) "T4RNA", should be "T4 RNA"; (page 38, line 5) "regions" should be "region".

Appropriate correction is required.

Several sentences in the specification lack clarity in their construction: (page 3, lines 25-26) "Also the recombination of the translation domain . . ."; (page 4, lines 18-20) "The human cells may be cells delivered from the human body . . ."; (page 5, lines 3-4) " . . . the search of **the** protein data base . . ."; (page 5, lines 21-22) "In general, the polymorphism due to the individual difference . . ."; (page 13, line 1) " . . . possible to immune responses, in a number of ways." Appropriate correction of these sentences is required to improve clarity.

The disclosure is objected to because of the following informalities: a blank section on page 16 in lines 9-10.

Appropriate correction is required.

The disclosure is objected to because of the following informalities: the DNA sequence and protein are repeatedly referred to in the specification without an associated sequence identification number (For example, see: page 4, lines 11-14, and 29; page 5, lines 1,12, and 15; page 38, lines 8, 9, and 14); the chimeric DNA-RNA oligonucleotide has no sequence identification number associated with it (page 35, lines 11-13).

Appropriate correction is required.

The disclosure is objected to because of the following informalities: no sequence identification number is given in Table 1, page 39. Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

> Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefor, subject to the conditions and requirements of this title.

Claim 1 is rejected under 35 U.S.C. 101 because the claimed invention is not supported by either a specific and substantial asserted utility or a well-established utility.

The claimed protein is not supported by either a specific and substantial utility or a well established utility because the specification fails to assert any utility for the protein and neither the specification as filed nor any art of record disclose or suggest any activity for the protein such that any utility would be well established for the protein.

There are no disclosed utilities for the protein comprising the amino acid sequence of SEQ ID NO: 1, naturally-occurring amino acid sequences having any sequence identity to SEQ ID NO: 1, biologically active fragments of SEQ ID NO: 1, and immunogenic fragments of SEQ

ID NO: 1. Neither the specification nor any art of record teaches what the protein comprising SEQ ID NO: 1 is, how it functions, or a specific and well-established utility for any of the fragments claimed. Furthermore, the specification does not teach a relationship to any specific disease or establish any involvement in the etiology of any specific disease.

The specification proposes that the protein comprising SEQ ID NO: 1 is a human membrane antigen TM4 superfamily protein. The specification teaches (pages 1-2) that the type II membrane proteins having transmembrane domains at four sites are referred to as the TM4 superfamily. This includes such genes encoding CD9, CD37, CD53, or CD82 antigens wherein the specification teaches that all such antigens have been found to exist on the hemopoietic cell surface and have been used as markers recognizing the cell population. The specification further proposes that since these membrane antigens are expressed in a manner specific to certain "specified cells and cancer cells", antibodies prepared against such antigens can be utilized for a variety of diagnosis or as carriers for the drug delivery system. However, the only information provided in the specification regarding the nucleic acid encoding the protein of SEQ ID NO:1 (page 38), as exemplified by SEQ ID NO: 2, is that the open reading frame codes for a protein consisting of 253 amino acids with a 32.5 % homology to the human CD63 antigen.

However, evidence based on protein sequence homology does not alone permit extrapolation to an isolated amino acid's biological function or use thereof. Bowie *et al.* (Science, 1990, 257:1306-1310) teach that an amino acid sequence encodes a message that determines the shape and function of a protein and that it is the ability of these proteins to fold into unique three-dimensional structures that allows them to function and carry out the instructions of the genome and further teaches that the problem of predicting protein structure

from sequence data and in turn utilizing predicted structural determinations to ascertain functional aspects of the protein is extremely complex. (Col. 1, p. 1306). Bowie *et al.* further teach that while it is known that many amino acid substitutions are possible in any given protein, the position within the protein's sequence where such amino acid substitutions can be made with a reasonable expectation of maintaining function are limited. Certain positions in the sequence are critical to the three dimensional structure/function relationship and these regions can tolerate only conservative substitutions or no substitutions (col. 2, p. 1306). The sensitivity of proteins to alterations of even a single amino acid in a sequence are exemplified by Burgess *et al.* (J of Cell Bio. 111:2129-2138, 1990) who teach that replacement of a single lysine reside at position 118 of acidic fibroblast growth factor by glutamic acid led to the substantial loss of heparin binding, receptor binding and biological activity of the protein and by Lazar *et al.* (Molecular and Cellular Biology, 1988, 8:1247-1252) who teach that in transforming growth factor alpha, replacement of aspartic acid at position 47 with alanine or asparagine did not affect biological activity while replacement with serine or glutamic acid sharply reduced the biological activity of the mitogen. These references demonstrate that even a single amino acid substitution will often dramatically affect the biological activity and characteristics of a protein. Thus, despite proposed homology between the protein comprising SEQ ID NO: 1 and the human membrane antigen TM4 superfamily of proteins, it cannot be predicted, based on the information in the specification, what affect this difference has on the function of the protein. Further even if the polypeptide of SEQ ID NO: 1 human membrane antigen TM4 superfamily protein, neither the specification nor any art of record teaches what the polypeptide is, what it does, nor teach a relationship to any

specific disease or establish any involvement of the polypeptide in the etiology of any specific disease or teach which fragments might be active as claimed in a pharmaceutical composition.

In addition, Bork (Genome Research, 2000,10:398-400) clearly teaches the pitfalls associated with comparative sequence analysis for predicting protein function because of the known error margins for high-throughput computational methods. Bork specifically teaches that computational sequence analysis is far from perfect, despite the fact that sequencing itself is highly automated and accurate (p. 398, col. 1). One of the reasons for the inaccuracy is that the quality of data in public sequence databases is still insufficient. This is particularly true for data on protein function. Protein function is context dependent, and both molecular and cellular aspects have to be considered (p. 398, col. 2). Conclusions from the comparison analysis are often stretched with regard to protein products (p. 398, col. 3). Furthermore, recent studies show that alternative splicing might affect more than 30% of human genes and the number of known post-translational modifications of gene products is increasing constantly so that complexity at protein level is enormous. Each of these modifications may change the function of respective gene products drastically (p. 399, col. 1). Further, although gene annotation via sequence database searches is already a routine job, even here the error rate is considerable (p. 399, col. 2). Most features predicted with an accuracy of greater than 70% are of structural nature and at best only indirectly imply a certain functionality (see legend for table 1, page 399). As more sequences are added and as errors accumulate and propagate it becomes more difficult to infer correct function from the many possibilities revealed by database search (p. 399, paragraph bridging cols. 2 and 3). The reference finally cautions that although the current methods seem to capture important features and explain general trends, 30% of those features are missing or

predicted wrongly. This has to be kept in mind when processing the results further (p. 400, paragraph bridging cols. 1 and 2). Clearly, given not only the teachings of Bowie *et al.*, Lazar *et al.* and Burgess *et al.*, but also the limitations and pitfalls of using computational sequence analysis and the unknown effects of alternative splicing, post translational modification and cellular context on protein function as taught by Bork, the function of the SEQ ID NO: 1 polypeptide can not be predicted.

The specification essentially gives an invitation to experiment wherein the artisan is invited to elaborate a functional use for the disclosed polypeptide and fragments thereof. Because the claimed invention is not supported by a specific asserted utility for the reasons set forth, credibility of any utility cannot be assessed.

Furthermore, claim 1, as written, does not sufficiently distinguish over proteins, as they exist naturally because the claims do not particularly point out any non-naturally occurring differences between the claimed products and the naturally occurring products. In the absence of the hand of man, the naturally occurring products are considered non-statutory subject matter. *See Diamond v. Chakrabarty*, 447 U.S. 303, 206 USPQ 193 (1980). The claims should be amended to indicate the hand of the inventor, e.g., by insertion of "Isolated" or "Purified". See MPEP 2105.

Thus, rejection of claim 1 under 35 U.S.C. 101 is deemed proper.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Firstly, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth in the rejections under 35 USC 101, one skilled in the art clearly would not know how to use the claimed invention as required under the first paragraph of 35 U.S.C. 112.

Furthermore, claim 1 is rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. The written description in this case only sets forth a protein comprising a protein encoded by SEQ ID NO: 1 and therefore the written description is not commensurate in scope with the claims which read on a protein comprising an deletions, substitutions, or additions of at least one amino acid residue.

The claim is drawn to a protein having sequence identity with a particular disclosed sequence. The claims do not require that the protein possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to a genus of proteins that is defined only by sequence identity.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing and identifying characteristics of the genus. The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factors present in the specification are the length of the protein and that it possesses four transmembrane domains. Further, there is no indication of what regions can be deleted, substituted, or added to such that

activity and structure are retained. Accordingly, in the absence of sufficient recitation of distinguishing and identifying characteristics, the specification does not provide adequate written description of the claimed genus.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession *of the invention*. The invention is, for purposes of the 'written description' inquiry, *whatever is now claimed.*" (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See *Vas-Cath* at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In *Fiddes*, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Therefore, only an isolated polypeptide comprising the amino acid sequence encoded by SEQ ID NO: 1, but not the full breadth of the claim meets the written description provision of 35 U.S.C. 112, first paragraph. Applicant is reminded that *Vas-Cath* makes clear that the written

description provision of 35 U.S.C. 112 is severable from its enablement provision (see page 1115).

Thus, rejection of this claim under the first paragraph of 35 U.S.C. 112 is deemed proper.

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claim 1 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The claim is drawn to a protein comprising an amino aid sequence represented by SEQ ID NO: 1. However, SEQ ID NO: 1 is presented in the sequence listing as a DNA sequence. Protein and DNA are structurally and functionally distinct molecules with unique functions within a cell. The discrepancy between the molecule claimed and that listed in the sequence listing renders the claim indefinite as to the actual claimed invention.

Furthermore, the term "at least" used in claim 1 to describe the number of potential amino acid changes in the claimed protein is a relative term which also renders the claim indefinite. The term "at least" is not defined by the claim, the specification does not provide a standard for ascertaining the requisite degree, and one of ordinary skill in the art would not be reasonably apprised of the scope of the invention.

Thus, rejection of this claim under the second paragraph of 35 U.S.C. 112 is deemed proper.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless -
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

Due to the indefiniteness nature of the claimed protein as set forth above (112 2nd paragraph), it was assumed for examination purposes that claim 1 encompasses a protein comprising an amino acid sequence ***encoded*** *by a polynucleotide comprising SEQ ID NO: 1.*

Claim 1 is rejected under 35 U.S.C. 102(e) as being anticipated by US Patent No. 6054289 (Moore, P. August 30, 1995).

The claim is drawn to a protein comprising an amino acid sequence encoded by SEQ ID NO: 1. Moore, P. teaches an isolated polypeptide comprising an amino sequence encoded by a polynucleotide of SEQ ID NO: 1. The amino acid sequence of SEQ ID NO: 17 taught by Moore, P. is 98% similar to the amino acid sequence encoded by the polynucleotide of SEQ ID NO: 1. (See sequence listing SEQ ID NO: 17, Cols. 61-64 and attached sequence comparison). Moore, P. further teaches (Col. 5, lines 5-10) that the invention of US Patent No. 6,054,289, " . . . is directed to polynucleotides having at least a 70% identity, preferably at least 90% and more preferably at least a 95% identity to polynucleotides which encode the polypeptides of SEQ ID NOS: 12-22, as well as fragments thereof, which fragments have at least 30 bases and preferably at least 50 bases and to polypeptides encoded by such polynucleotides." Thus, rejection of claim 1 under 35 U.S.C. 102 is deemed proper.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Peter J. Reddig whose telephone number is (571) 272-9031. The examiner can normally be reached on M-F 8:30 a.m.-5:00 p.m..

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Jeffrey Siew can be reached on (571) 272-0787. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Peter J. Reddig, Ph.D.
Examiner
Art Unit 1642

PJR

GARY B. NICKOL, PH.D.
PRIMARY EXAMINER

GenCore version 5.1.7

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:31:55 ; Search time 7.5 Seconds
(without alignments)
1673.356 Million cell updates/sec

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Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1300	91.0	252	2	US-08-705-771-17	Sequence 17, Appl
2	1300	91.0	252	2	US-09-417-540-17	Sequence 17, Appl
3	453	31.7	222	2	US-10-037-417-81	Sequence 81, Appl
4	344	24.1	253	2	US-09-333-599-4	Sequence 4, Appli
5	344	24.1	253	2	US-09-499-781-4	Sequence 4, Appli
6	343.5	24.0	249	2	US-09-949-016-8334	Sequence 8334, Ap
7	333.5	23.3	267	2	US-09-949-016-9088	Sequence 9088, Ap
8	333.5	23.3	275	2	US-09-949-016-8346	Sequence 8346, Ap
9	332	23.2	253	2	US-09-333-599-2	Sequence 2, Appli
10	332	23.2	253	2	US-09-499-781-2	Sequence 2, Appli
11	332	23.2	276	2	US-09-949-016-8972	Sequence 8972, Ap
12	329	23.0	245	2	US-10-012-231A-4	Sequence 4, Appli
13	329	23.0	245	2	US-10-015-389A-4	Sequence 4, Appli
14	329	23.0	245	2	US-10-006-768A-4	Sequence 4, Appli
15	329	23.0	245	2	US-10-015-671A-4	Sequence 4, Appli
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18	329	23.0	245	2	US-10-006-041A-4	Sequence 4, Appli
19	329	23.0	245	2	US-10-012-064A-4	Sequence 4, Appli
20	303	21.2	255	2	US-09-949-016-9861	Sequence 9861, Ap
21	301.5	21.1	238	2	US-09-949-016-6334	Sequence 6334, Ap
22	299.5	21.0	222	2	US-09-949-016-8347	Sequence 8347, Ap
23	297.5	20.8	260	2	US-09-949-016-7296	Sequence 7296, Ap
24	297.5	20.8	270	2	US-09-949-016-9117	Sequence 9117, Ap
25	285	19.9	265	1	US-08-807-044-1	Sequence 1, Appli
26	283	19.8	267	2	US-08-430-225A-20	Sequence 20, Appl
27	283	19.8	267	2	US-09-795-380-20	Sequence 20, Appl
28	273.5	19.1	219	1	US-08-855-140-3	Sequence 3, Appli
29	273.5	19.1	219	1	US-08-807-044-3	Sequence 3, Appli
30	273.5	19.1	219	4	PCT-US91-04986-2	Sequence 2, Appli
31	273.5	19.1	231	2	US-09-949-016-10626	Sequence 10626, A
32	271	19.0	280	1	US-08-855-140-1	Sequence 1, Appli
33	270.5	18.9	219	1	US-08-855-140-4	Sequence 4, Appli
34	263	18.4	241	2	US-08-808-148-1	Sequence 1, Appli
35	263	18.4	241	2	US-09-020-956-114	Sequence 114, App
36	263	18.4	241	2	US-09-030-607-114	Sequence 114, App
37	263	18.4	241	2	US-09-439-313-114	Sequence 114, App
38	263	18.4	241	2	US-09-352-616A-114	Sequence 114, App
39	263	18.4	241	2	US-09-232-149A-114	Sequence 114, App
40	263	18.4	241	2	US-09-159-812-114	Sequence 114, App
41	263	18.4	241	2	US-09-636-215-114	Sequence 114, App
42	263	18.4	241	2	US-09-685-166A-114	Sequence 114, App
43	263	18.4	241	2	US-09-115-453-114	Sequence 114, App
44	263	18.4	241	2	US-09-688-489-114	Sequence 114, App
45	263	18.4	241	2	US-09-679-426-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-08-705-771-17
; Sequence 17, Application US/08705771
; Patent No. 6054289
; GENERAL INFORMATION:
; APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
; APPLICANT: Jian Ni and Jing-Shan Hu
; TITLE OF INVENTION: Human Genes, Sequences and
; TITLE OF INVENTION: Expression Products
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/705,771
; FILING DATE: August 30, 1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 973-994-1700
; TELEFAX: 973-994-1744
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:

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;      LENGTH:  252 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-705-771-17

Alignment Scores:
Pred. No.:              4.65e-138      Length:         252
Score:                  1300.00        Matches:        252
Percent Similarity:     98.8%          Conservative:   0
Best Local Similarity:  98.8%          Mismatches:     0
Query Match:            91.0%          Indels:         3
DB:                     2              Gaps:           0

US-10-608-388A-1 (1-759) x US-08-705-771-17 (1-252)

Qy          1 ATGGGCCAGTGCGGCATCACCTCCTCCAAGACCGTGCTGGTCTTTCTCAACCTCATCTTC 60
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Db          1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20

Qy         61 TGGGGGGCAGCTGGCATTTTATGCTATGTGGGAGCCTATGTCTTCATCACTTATGATGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40

Qy        121 TATGACCACTTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGATCATAGCTGTA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleIleAlaVal 60

Qy        181 GGAGCCCTGCTTTTCATCATTGGGCTAATTGGCTGCTGTGCCACAATCCGGGAAAGTCGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80

Qy        241 TGTGGACTTGCCACGTTTGTCATCATCCTGCTCTTGGTTTTTGTCACAGAAGTTGTTGTA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100

Qy        301 GTGGTTTTGGGATATGTTTACAGAGCAAAGGTGGAAAATGAGGTTGATCGCAGCATTCAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120

Qy        361 AAAGTGTATAAGACCTACAATGGAACCAACCCTGATGCTGCTAGCCGGGCTATTGATTAT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140

Qy        421 GTACAGAGACAGCTGCATTGTTGTGGAATTCACAACTACTCAGACTGGGAAAATACAGAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160

Qy        481 TGGTTCAAAGAAACCAAAAACCAGAGTGTCCCTCTTAGCTGCTGCAGAGAGACTGCCAGC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180

Qy        541 AATTGTAATGGCAGCCTGGCCCACCCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
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Db        181 AsnCysAsnGlySer-Trp-ProProPheArg-LeuTyrAlaGluGlyCysGluAlaLeu 199

Qy        601 GTAGTGAAGAAGCTACAAGAAATCATGATGCATGTGATCTGGGCCGCACTGGCATTTGCA 660
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Db        200 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 219

Qy        661 GCTATTCAGCTGCTGGGCATGCTGTGTGCTTGCATCGTGTTGTGCAGAAGGAGTAGAGAT 720
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Db        220 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 239

Qy        721 CCTGCTTACGAGCTCCTCATCACTGGCGGAACCTATGCA 759
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Db        240 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 252

RESULT 2
US-09-417-540-17
; Sequence 17, Application US/09417540
; Patent No. 6639052
;   GENERAL INFORMATION:
;       APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
;                  Jian Ni and Jing-Shan Hu
;       TITLE OF INVENTION: Human Genes, Sequences and
;                           Expression Products
;       NUMBER OF SEQUENCES: 22
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
;                       CECCHI, STEWART & OLSTEIN
;            STREET: 6 BECKER FARM ROAD
;            CITY: ROSELAND
;            STATE: NEW JERSEY
;            COUNTRY: USA
;            ZIP: 07068
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: 3.5 INCH DISKETTE
;            COMPUTER: IBM PS/2
;            OPERATING SYSTEM: MS-DOS
;            SOFTWARE: WORD PERFECT 5.1
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/417,540
;            FILING DATE: 14-Oct-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/705,771
;            FILING DATE: August 30, 1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: MULLINS, J.G.
;            REGISTRATION NUMBER: 33,073
;            REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 973-994-1700
;            TELEFAX: 973-994-1744
;   INFORMATION FOR SEQ ID NO: 17:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 252 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-417-540-17

Alignment Scores:
Pred. No.:              4.65e-138      Length:         252
Score:                  1300.00        Matches:        252
Percent Similarity:     98.8%          Conservative:   0
Best Local Similarity:  98.8%          Mismatches:     0
Query Match:            91.0%          Indels:         3
DB:                     2              Gaps:           0

US-10-608-388A-1 (1-759) x US-09-417-540-17 (1-252)

Qy          1 ATGGGCCAGTGCGGCATCACCTCCTCCAAGACCGTGCTGGTCTTTCTCAACCTCATCTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20

Qy         61 TGGGGGGCAGCTGGCATTTTATGCTATGTGGGAGCCTATGTCTTCATCACTTATGATGAC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40

Qy        121 TATGACCACTTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGATCATAGCTGTA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleIleAlaVal 60

Qy        181 GGAGCCCTGCTTTTCATCATTGGGCTAATTGGCTGCTGTGCCACAATCCGGGAAAGTCGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80

Qy        241 TGTGGACTTGCCACGTTTGTCATCATCCTGCTCTTGGTTTTTGTCACAGAAGTTGTTGTA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100

Qy        301 GTGGTTTTGGGATATGTTTACAGAGCAAAGGTGGAAAATGAGGTTGATCGCAGCATTCAG 360
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